

## SEQUENCE LISTING

<110> Evans, Ronald M.  
                  Blumberg, Bruce

<120> NOVEL STEROID-ACTIVATED NUCLEAR  
RECEPTORS AND USES THEREFOR

<130> SALK2270-2

<140> 09/458,366  
<141> 1999-12-09

<150> 09/005,286  
<151> 1998-01-09

<160> 39

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<222> (583) . . . (1884)

<223> N is selected from A, C, T/U or G

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ccttttcctg tgaaaaatgt gtgaagagac ctgaaaagaaa aaagttaggga gaacataatg	180	
agaacaata cggtaatctc ttcatttgct agttcaagtg ctggacttgg gacttaggag	240	
gggcaatggc gcccgttagt gcctacatct gacttggact gaaatatagg tgagagacaa	300	
gattgtctca tatccgggaa aatcataacc tatgacttagg acgggaagag gaagcactgc	360	
ctttacttca gtggaaatct cggcctcagc ctgcaagcca agtgttcaca gtgagaaaaag	420	
caagagaata agctaatact cctgtcctga acaaggcagc ggctccttgg taaagctact	480	
ccttgatcga tcctttgcac cggattgttc aaagtggacc ccaggggaga agtcggagca	540	
aagaacttac caccaagcag tccaaagaggc ccagaagcaa ac ctg gag gtg aga	594	
	Leu Glu Val Arg	

ccc aaa gaa agc tgg aac cat gct gac ttt gta cac tgt gag gac aca  
 Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His Cys Glu Asp Thr  
       5            10            15            20

gag tct gtt cct gga aag ccc agt gtc aac gca gat gag gaa gtc gga 690  
Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp Glu Glu Val Gly  
25 30 35

ggc ccc caa atc tgc cgt gta tgt ggg gac aag gcc act ggc tat cac  
 Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala Thr Gly Tyr His  
 40                  45                  50

ttc aat gtc atg aca tgt gaa gga tgc aag ggc ttt ttc agg agg agg gcc  
Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ala 786

55	60	65	
atg aaa cgc aac gcc cg <sup>g</sup> ctg agg tgc ccc ttc cg <sup>g</sup> aag ggc gcc tgc Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg Lys Gly Ala Cys	70	75	834
		80	
gag atc acc cg <sup>g</sup> aag acc cg <sup>g</sup> cga cag tgc cag gcc tgc cg <sup>c</sup> ctg cg <sup>c</sup> Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala Cys Arg Leu Arg	85	90	882
		95	
aag tgc ctg gag agc gg <sup>c</sup> atg aag gag atg atc atg tcc gac gag Lys Cys Leu Glu Ser Gly Met Lys Glu Met Ile Met Ser Asp Glu	105	110	930
		115	
gcc gtg gag gag agg cg <sup>g</sup> gcc ttg atc aag cg <sup>g</sup> aag aaa agt gaa cg <sup>c</sup> Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys Ser Glu Arg	120	125	978
		130	
aca ggg act cag cca ctg gga gtg cag ggg ctg aca gag gag cag cg <sup>c</sup> Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr Glu Glu Gln Arg	135	140	1026
		145	
atg atg atc agg gag ctg atg gac gct cag atg aaa acc ttt gac act Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr	150	155	1074
		160	
acc ttc tcc cat ttc aag aat ttc cg <sup>g</sup> ctg cca ggg gtg ctt agc agt Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser	165	170	1122
		175	
ggc tgc gag ttg cca gag cct ctg cag gcc cca tcg agg gaa gaa gct Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser Arg Glu Glu Ala	185	190	1170
		195	
gcc aag tgg agc cag gtc cg <sup>g</sup> aaa gat ctg tgc tct ttg aag gtc tct Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser	200	205	1218
		210	
ctg caa gct gcg ggg gga tgg cag tgt ctg gaa cta caa acn ccc Leu Gln Ala Ala Gly Gly Trp Gln Cys Leu Glu Leu Gln Xaa Pro	215	220	1266
		225	
agc cga cag tgg cg <sup>g</sup> aaa gag atc ttc tcc ctg ctg ccc cac atg gct Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala	230	235	1314
		240	
gac atg tca acc tac atg ttc aaa ggc atc atc agc ttt gcc aaa gtc Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val	245	250	1362
		255	
atc tcc tac ttc agg gag ttc ccc atc gag gac cag atc tcc ctg ctg Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu	265	270	1410
		275	
aag ggg gcc gct ttc gag ctg tgt caa ctg aga ttc aac aca gtg ttg Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe	280	285	1458
		290	
aac gcg gag act gga acc tgg gag tgt ggc cg <sup>g</sup> ctg tcc tac tgc ttg Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu			1506

295

300

305

gaa gac act gca ggt ggc ttc cag caa ctt cta ctg gag ccc atg ctg Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu 310	315	320	1554
aaa ttc cac tac atg ctg aag aag ctg cag ctg cat gag gag gag tat Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr 325	330	335	1602
gtg ctg atg cag gcc atc tcc ctc ttc tcc cca gac cgc cca ggt gtg Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val 345	350	355	1650
ctg cag cac cgc gtg gtg gac cag ctg cag gag caa ttc gcc att act Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr 360	365	370	1698
ctg aag tcc tac att gaa tgc aat cgg ccc cag cct gct cat agg ttc Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe 375	380	385	1746
ttg ttc ctg aag atc atg gct atg ctc acc gag ctc cgc agc atc aat Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn 390	395	400	1794
gct cag cac acc cag cgg ctg ctg cgc atc cag gac ata cac ccc ttt Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe 405	410	415	1842
gct acg ccc ctc atg cag gag ttg ttc ggc atc aca ggt agc Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr Gly Ser 425	430		1884
ttagcggtctg ccttgggtga caccttcgag aggcagccag acccagagcc ctctgagccg gcactcccgg gccaagacag atggacactg ccaagagccg acaatgcctt gctggcctgt ctccctaggg aattcctgct atgacagctg gctagcattc ctcaggaagg acatgggtg cccc			1944 2004 2064 2068
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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala 35 40 45			
Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe 50 55 60			
Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg 65 70 75 80			
Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala 85 90 95			

Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile  
 100 105 110  
 Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys  
 115 120 125  
 Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr  
 130 135 140  
 Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys  
 145 150 155 160  
 Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly  
 165 170 175  
 Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser  
 180 185 190  
 Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser  
 195 200 205  
 Leu Lys Val Ser Leu Gln Ala Ala Gly Gly Trp Gln Cys Leu Glu  
 210 215 220  
 Leu Gln Xaa Pro Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu  
 225 230 235 240  
 Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser  
 245 250 255  
 Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln  
 260 265 270  
 Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe  
 275 280 285  
 Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu  
 290 295 300  
 Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu  
 305 310 315 320  
 Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His  
 325 330 335  
 Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp  
 340 345 350  
 Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln  
 355 360 365  
 Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro  
 370 375 380  
 Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu  
 385 390 395 400  
 Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp  
 405 410 415  
 Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr  
 420 425 430  
 Gly Ser

<210> 3  
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 hydroxylase, rCYP3A1

<400> 3  
 tagacagttc atgaagttca tctac

<210> 4  
 <211> 25  
 <212> DNA

<213> Artificial Sequence

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<223> putative SXR response element from the steroid hydroxylase, rCYP3A2

<400> 4 taagcagttc ataaagttca tctac 25

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> putative SXR response element from the steroid hydroxylase, rUGT1A6

<400> 5 actgttagttc ataaagttca catgg 25

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> putative SXR response element from the steroid hydroxylase, rbCYP2C1

<400> 6 caatcagttc aacagggttc accaat 26

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> putative SXR response element from the steroid hydroxylase, rP450R

<400> 7 cacaggtgag ctgaggccag cagcaggtcg aaa 33

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> putative SXR response element from the steroid hydroxylase, rCYP2A1

<400> 8 gtgcaggttc aactggaggt caacatg 27

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> putative SXR response element from the steroid  
hydroxylase, rCYP2A2

<400> 9

gtgctggttc aactggaggt cagtatg

27

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> putative SXR response element from the steroid  
hydroxylase, rCYP2C6

<400> 10

agtctagttc agtgggggtt cagtctt

27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> putative SXR response element from the steroid  
hydroxylase, hCYP2E1

<400> 11

gagatggttc aaggaagggt cattaac

27

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> direct repeat with spacer of 0 nucleotides

<400> 12

catagtcagg tcaaggtagc atcaac

26

<210> 13

<211> 27

<212> DNA

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<223> direct repeat with spacer of 1 nucleotides

<400> 13

catagtcagg tcataaggta gatcaac

27

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

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<400> 14
catagtcagg tcaataggc agatcaac 28

<210> 15
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<400> 15
catagtcagg tcatataggt cagatcaac 29

<210> 16
<211> 30
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<400> 16
catagtcagg tcatataagg tcagatcaac 30

<210> 17
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> direct repeat with spacer of 5 nucleotides

<400> 17
catagtcagg tcatatatag gtcagatcaa c 31

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> direct repeat with spacer of 6 nucleotides

<400> 18
catagtcagg tcatatataa ggtcaagatc aac 33

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> direct repeat with spacer of 7 nucleotides

<400> 19
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<210> 20  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> direct repeat with spacer of 10 nucleotides

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36

<210> 21  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 21  
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41

<210> 22  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> repeat\_unit  
<222> (7)...(7)  
<223> N is a nucleotide spacer of 3, 4 or 5 nucleotides,  
wherein each N is independently selected from A,  
T, C or G

<223> example of a response element suitable for  
practice of the invention method

<400> 22  
agtccatgtc act

13

<210> 23  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> repeat\_unit  
<222> (7)...(7)  
<223> N is a nucleotide spacer of 6 nucleotides, wherein  
each N is independently selected from A, T, C or G

<223> example of a response element suitable for  
practice of the invention method

<400> 23  
tgaactnagg tca

13

<210> 24  
<211> 18

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> inverted repeat with 6 nucleotide spacer found in  
 CYP3A4

<400> 24  
 tgaactcaaa ggaggtca

<210> 25  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> inverted repeat response element with spacer of 0  
 nucleotides

<400> 25  
 agcttaggtc atgaccta

18

<210> 26  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> inverted repeat response element with spacer of 1  
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<400> 26  
 agcttaggtc agtgaccta

19

<210> 27  
 <211> 20  
 <212> DNA  
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 <223> inverted repeat response element with spacer of 2  
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<400> 27  
 agcttaggtc acgtgaccta

20

<210> 28  
 <211> 21  
 <212> DNA  
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<220>  
 <223> inverted repeat response element with spacer of 3  
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<400> 28  
 agcttaggtc acagtgaccta a

21

<210> 29  
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<212> DNA  
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<400> 29  
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22

<210> 30  
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<400> 30  
 agcttaggtc acactgtgac cta

23

<210> 31  
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<220>  
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<400> 31  
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23

<210> 32  
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<220>  
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<400> 32  
 agcttacgtc atgacgta

18

<210> 33  
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 <212> DNA  
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 <223> CYP3A oligonucleotide, CYP3A4, tested for binding

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33

<210> 34  
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<220>  
<223> CYP3A oligonucleotide, CYP3A5, tested for binding

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<210> 35  
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<220>  
<223> CYP3A oligonucleotide, CYP3A7, tested for binding

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<210> 36  
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<220>  
<223> oligonucleotide for PCR

<400> 36  
gagcaattcg ccattactct gaagt 25

<210> 37  
<211> 25  
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<213> Artificial Sequence

<220>  
<223> oligonucleotide for PCR

<400> 37  
gtccttgggg tcttctacct ttctc 25

<210> 38  
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<400> 38  
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<210> 39  
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<220>  
<223> oligonucleotide for PCR

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